

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 1999, 23:01:43 ; Search time 360.53 Seconds  
(without alignments)  
621.966 Million cell updates/sec

Title: US-09-205-015-2  
Perfect score: 147  
Sequence: 1 agataactgggcaaccatg.....ctcccccctctgtttatct 147

Scoring table: IDENTITY\_NUC

Searched: 2002476 seqs, 762712212 residues

Database : EST:\*

1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
7: em\_est7:\*  
8: em\_est8:\*  
9: em\_est9:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: gb\_est6:\*  
16: gb\_est7:\*  
17: gb\_est8:\*  
18: gb\_est9:\*  
19: gb\_est10:\*  
20: gb\_est11:\*  
21: gb\_est12:\*  
22: gb\_est13:\*  
23: gb\_est22:\*  
24: gb\_est14:\*  
25: gb\_est15:\*  
26: gb\_est16:\*  
27: gb\_est17:\*  
28: gb\_est18:\*  
29: gb\_est19:\*  
30: gb\_est20:\*  
31: gb\_est21:\*  
32: em\_est10:\*  
33: em\_est11:\*  
34: em\_est12:\*  
35: em\_est13:\*  
36: em\_est14:\*  
37: em\_est15:\*  
38: em\_est16:\*  
39: em\_est17:\*  
40: em\_est18:\*  
41: em\_est19:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33.2	22.6	443	17	HSPD04245 F19640 H.sapiens E
2	30.6	20.8	447	24	AA646832 vn37d04.r

C	3	30.4	20.7	381	11	H51183
C	4	29.8	20.3	447	11	R87592
	5	29.4	20.0	363	28	AA893137
	6	29.2	19.9	539	10	R18712
	7	29.2	19.9	295	27	AA819433
	8	29.2	19.9	535	27	AA874935
	9	29.2	19.9	413	27	AA892220
	10	29.2	19.9	454	28	AA801097
	11	29.2	19.9	573	28	AI009661
	12	29.2	19.9	522	30	AI105198
	13	29	19.7	425	19	HSPD06480
C	14	28.8	19.6	579	16	AA204345
	15	28.8	19.6	544	21	AA293284
	16	28.6	19.5	409	14	T15281
C	17	28.4	19.3	484	11	R62406
	18	28.4	19.3	195	12	H81967
C	19	28.4	19.3	412	19	AA400586
	20	28.4	19.3	243	27	H34430
C	21	28.2	19.2	634	14	AA028226
C	22	28.2	19.2	444	14	W42291
	23	28.2	19.2	619	14	W52157
C	24	28.2	19.2	720	16	AA108435
C	25	28.2	19.2	676	16	AA218243
C	26	28.2	19.2	307	17	AA267667
C	27	28.2	19.2	251	17	AA270488
C	28	28.2	19.2	466	17	AA272879
C	29	28.2	19.2	376	20	AA466633
C	30	28.2	19.2	478	20	AA475090
C	31	28.2	19.2	506	20	AA492778
C	32	28.2	19.2	546	21	AA543228
C	33	28.2	19.2	354	23	AI216242
C	34	28.2	19.2	439	24	AA656473
C	35	28.2	19.2	296	31	AI232782
	36	28	19.0	395	19	HSPD05706
	37	28	19.0	356	21	AA39298
C	38	27.8	18.9	316	11	T29869
	39	27.8	18.9	483	12	N40183
C	40	27.8	18.9	348	14	W37314
	41	27.8	18.9	577	15	AA143783
	42	27.8	18.9	436	23	AI270351
	43	27.8	18.9	400	24	T04238
	44	27.8	18.9	439	26	AA776241
	45	27.8	18.9	764	29	AI052032

#### ALIGNMENTS

#### RESULT 1

HSPD04245

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

ORGANISM

HSPD04245 443 bp DNA EST 21-APR-1997  
H.sapiens EST sequence (011-X4-12) from skeletal muscle, mRNA  
Sequence.  
F19640  
g1136055  
EST.  
human.  
Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;  
Homo.  
1 (bases 1 to 443)  
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A.,  
Pandolfo,D., Toppo,S., Trevisan,S., Scarsio,S. and Valle,G.  
Identification of 4,370 expressed sequence tags (ESTs) from a  
3'-end specific cDNA library of human skeletal muscle by DNA  
sequencing and filter hybridisation  
Genome Res. 1, 35-42 (1996)  
2 (bases 1 to 443)  
Valle,G.  
Direct Submission  
Submitted (19-DEC-1995) CRIBI Biotechnology Centre, University of  
Padua, Via Trieste 75, 35121 Padua, Italy

COMMENT ABI Chromatograms and other information are available on WWW at <http://eos.bio.unipd.it>  
 Vector: pcDNAII (Invitrogen)  
 V.type: Plasmid  
 RE\_1: EcoRI  
 RE\_2: NotI  
 PRIMER: PC2R  
 DESC: The cDNA was constructed using a biotin-NotI-oligo(dT) primer, sonicated and size selected (450-550 bp). The biotinylated 3'-ends were affinity purified, directionally cloned and sequenced (5' -> 3').

FEATURES  
 source Location/Qualifiers  
 1. .443  
 /organism="Homo sapiens"  
 /note="caucasian"  
 /db\_xref="taxon:9606"  
 /tissue\_type="pectoral muscle (after mastectomy)"  
 /clone\_lib="HMI"  
 /sex="female"  
 BASE COUNT 92 a 147 c 101 g 102 t 1 others  
 ORIGIN

Query Match 22.6%; Score 33.2; DB 17; Length 443;  
 Best Local Similarity 55.9%; Pred. NO. 1.9;  
 Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
 QY 35 gagccacaggaactctgagctatcctgtgggtgaggtgggacaaaggggt 94  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 276 GAGGCACTGGGGNTCTCAGCCACCCCGTGTAAACAAGTGGAGGAGGGGGT 335  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 95 gaatggtactctgattacacacctgtgtgctgcctccctcctctgttat 145  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 336 GGAGACACCTTTCTCCAGCCCTGTGTCACACACCTCTTTTGTGT 386  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2  
 AA646832/c 447 bp mRNA EST 28-OCT-1997  
 LOCUS vn37404.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone  
 DEFINITION 1023567 5', mRNA sequence.  
 ACCESSION AA646832  
 NID 92573261  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 447)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Streptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 MGI:574143  
 Seq primer: -28ml3 rev1 ET from Amersham.  
 FEATURES  
 source Location/Qualifiers  
 1. .447  
 /organism="Mus musculus"  
 /strain="C57BL/6"

/note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3' /db\_xref="taxon:10090"  
 /clone\_lib="Stratagene mouse skin (#937313)"  
 /sex="females"  
 /tissue\_type="whole skin"  
 /dev\_stage="11 weeks old"  
 /lab\_host="SOLR (kanamycin resistant)"  
 BASE COUNT 69 a 148 c 76 g 154 t  
 ORIGIN

Query Match 20.8%; Score 30.6; DB 24; Length 447;  
 Best Local Similarity 58.1%; Pred. No. 11;  
 Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
 QY 36 agggccacaggaactctgagctatcctgtgggtgaggtgggacaaaggggtg 95  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 125 AGAGCAGACTGAAGTCTGAGGAGCGCTGAGGAGCAGAGCTTGAGGAGGAGGAGCA 66  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 96 aatggtactctgattacacacctctgtgtgtgc 128  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 65 GAGGAACCTGTAGATAGAACCTCTGGGAGCGC 33

RESULT 3  
 H51183/c 381 bp mRNA EST 18-SEP-1995  
 LOCUS yo32ell.r1 Homo sapiens cDNA clone 179660 5'.  
 DEFINITION H51183  
 ACCESSION H51183  
 NID 9991024  
 KEYWORDS EST.  
 SOURCE human clone-179660 primer-M13RP1 library-Soares adult brain

N2B4HB55Y vector-pT7T3D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) Ksitel-Not I rsite2-Eco RI 55-year old male. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex areas of the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla.

ORGANISM Homo sapiens  
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 381)

REFERENCE 1 (bases 1 to 381)  
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108



```

Db 203 AGAATTGGCAGAAAGGCTCATGTATACAGAGGCCAGCTGCTCTTCTGCTCTCTCTG 262
Qy 63 gtgggggtgaggtgggacaaaggaaagggtgaatggtactgctgattacaacctctgg 122
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 263 TTGGGACAAGGGTAGTGAGAAGGTGAGAGGCGATAGCGGACTCTCTCCAGAAAATTGG 322
Qy 123 tggctgctccccctctctgtttatc 146
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 323 GGGCTCTCATGTCATCTGCATCNC 346

RESULT 6
R18712 539 bp mRNA EST 14-APR-1995
LOCUS Yf98f07.r1 Homo sapiens cDNA clone 30551 5' similar to SP:MEC2_RAT
DEFINITION Q00566 METHYL-CPG-BINDING PROTEIN 2 ;
ACCESSION R18712
NID 9772322
KEYWORDS EST.
SOURCE human clone-30551 library-Soares infant brain 1NIB vector-Lafmid BA
host-DH10B (ampicillin resistant) primer-M13RP1 Rsite1-Not I
Rsite2-Hind III Whole brain from a 73 days post natal female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
ACTGGAAGATTCGGCGCGAGGATTTTCTTTTCTTTT 3']; double-stranded
cDNA was ligated to Hind III adaptors (Pharmacia), digested with
Not I and directionally cloned into the Not I and Hind III sites of
the Lafmid BA vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.Fatima
Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,K., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT GDB: G00-402-898
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 458
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
    Location/Qualifiers
    1..539
    /organism="Homo sapiens"
    /clone="30551"
BASE COUNT 140 a 122 c 152 g 116 t 9 others
ORIGIN
Query Match 19.9%; Score 29.2; DB 10; Length 539;
Best Local Similarity 50.8%; Pred. No. 28;
Matches 67; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1 agtaactgggccaacatgactcagctgttctggaggccaacagactctgagtcac 60
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 AGAAGAAGAGGGCAAGCATGAGCCGCTGCAGCCATAGCCACCACCTCTGCTGAGCCGC 178
Qy 61 ctgtgggggtgggggtgggacaaaggaaagggtgaatggtactgctgattacaacctct 120
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 AGAGGAGGCAAGAGAGACATCAGAGGGTCAGGCTCCGCCCGGCTGTGGCAANGCT 238

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Qy 121 ggtgctgctcc 132
    ||||| | | | | |
Db 239 TCTGCTCCCCC 250

RESULT 7
AA819433 295 bp mRNA EST 09-MAR-1998
LOCUS UI-R-A0-bl-h-09-0-UI.s1 UI-R-A0 Rattus norvegicus cDNA clone
DEFINITION UI-R-A0-bl-h-09-0-UI 3' similar to gb|U13257|RATNAP12A Rattus
norvegicus, renal Na/Pi-cotransport mRNA, complete cds, mRNA
sequence.
ACCESSION AA819433
NID 92946932
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 295)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT On Mar 10, 1998 this sequence version replaced gi:2889522.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dT track (not shown) served to identify it as a clone from
the normalized adult kidney library. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
Seq primer: M13 Forward.
FEATURES
    Location/Qualifiers
    1..295
    /organism="Rattus norvegicus"
    /strain="Sprague-Dawley"
    /note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture."
    /db_xref="taxon:10116"
    /clone="UI-R-A0-bl-h-09-0-UI"
    /clone_lib="UI-R-A0"
    /dev_stage="adult"
    /lab_host="DH10B (Life Technologies)"
BASE COUNT 75 a 76 c 68 g 76 t
ORIGIN
Query Match 19.9%; Score 29.2; DB 27; Length 295;
Best Local Similarity 50.7%; Pred. No. 27;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 3 ataactggccaacatgactcagctgttctggaggccaacagactctgagtcac 62
    ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 47 AGAATTGGCAGAGGAGGCTCATGTATACAGAGGCCAGCTCTCTTCTGCTCTCTG 106
Qy 63 gtgggggtgaggtgggacaaaggaaagggtgaatggtactgctgattacaacctctg 122
    ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 107 TTGGGACAAGGGTAGTGAGAAGGTGAGAGGCGATAGCGGACTCTCTCCAGAAAATTGG 166

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Qy 123 tgcgtcctccccctctg 140
Db 167 GGGCTCCTCATGCATCTG 184

RESULT 8
AA874935 535 bp mRNA EST 20-MAR-1998
LOCUS UI-R-E0-ci-c-06-0-UI.s1 UI-R-E0 Rattus norvegicus cDNA clone
DEFINITION UI-R-E0-ci-c-06-0-UI 3' similar to gi1816434|dbj|AB000733|AB000733
ACCESSION AA874935
NID 92979683
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
TITLE 1 (bases 1 to 535)
JOURNAL Bonaldo,M.F., Lennon,G. and Soares,M.B.
MEDLINE Normalization and subtraction: two approaches to facilitate gene
COMMENT Genome Res. 6 (9), 791-806 (1996)
97044477

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dr track (not shown) served to identify it as a clone from
the normalized adult 12-day-embryo library. CDNA Library
Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones
will be available through Research Genetics
Seq primer: M13 Forward.

FEATURES
    source
        1..535
            /organism="Rattus norvegicus"
            /strain="Sprague-Dawley"
            /note="Vector: pT73D-Pac (Pharmacia) with a modified
            polylinker; Site_1: NotI; Site_2: EcoRI; This library
            consists of a mixture of individually tagged normalized
            libraries constructed from 8, 12 and 18-day embryo. The
            tag is a string of 3-5 nucleotides present between the
            Not I site and the oligo-dr track which allows
            identification of the library of origin of a clone within
            the mixture."
            /db_xref="taxon:10116"
            /clone="UI-R-E0-ci-c-06-0-UI"
            /clone_lib="UI-R-E0"
            /dev_stage="embryonic"
            /lab_host="DH10B (Life Technologies)"

BASE COUNT 156 a 123 c 113 g 143 t
ORIGIN

Query Match 19.9%; Score 29.2; DB 27; Length 535;
Best Local Similarity 59.8%; Pred. No. 28;
Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 49 ttctgagtcacctgtgggggtggaggaaggaaggggtgaatgtactctg 108
Db 46 TTCAGCGCAATAGCTTTGGAGGAATGGGACAGGGTAGGGTCTCAATGTAATGCTT 105
Qy 109 attacaacctctgtgtgctc 130
Db 106 ATTTCAGGTCCTTATGTAGCT 127

us-09-205-015-2.rst

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RESULT 9
AA892220 413 bp mRNA EST 03-APR-1998
LOCUS EST196023 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
DEFINITION RKIAN83 3' end, mRNA sequence.
ACCESSION AA892220
NID 93019099
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
TITLE 1 (bases 1 to 413)
JOURNAL Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
COMMENT Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
unpublished (1998)

Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES
    source
        1..413
            /organism="Rattus sp."
            /note="Organ: kidney; Vector: pT7T3pac; Site_1: EcoRI;
            Site_2: NotI"
            /db_xref="taxon:10118"
            /clone="RKIAN83"
            /clone_lib="Normalized rat kidney, Bento Soares"

BASE COUNT 111 a 112 c 93 g 97 t
ORIGIN

Query Match 19.9%; Score 29.2; DB 27; Length 413;
Best Local Similarity 50.7%; Pred. No. 27;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 3 ataactggggcaaccatcagtcagtcgtctgtggagggcaacaggagctctgagtcactc 62
Db 48 AGAATTGGCAGAGGAAGGCTCATGTATACAGAGGCCAGCTGCTCTCTGCGCTCTCTG 107
Qy 63 gtgggggtgagggtgggacaagggaagggtgaatgtactgtctgattacaaccttg 122
Db 108 TTGGACAAGGGTATGTAGAGAGGTGAGAGGGCATAGCGGACTCTTCCAGAAAATTTGG 167
Qy 123 tgcgtcctccccctctg 140
Db 168 GGGCTCCTCATGCATCTG 185

RESULT 10
AA801097 454 bp mRNA EST 30-APR-1998
LOCUS EST190594 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
DEFINITION ROVA54 3' end, mRNA sequence.
ACCESSION AA801097
NID 92864052
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
TITLE 1 (bases 1 to 454)
JOURNAL Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
COMMENT Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
unpublished (1998)

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RESULT 13  
HSPD06480

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ORGANISM      Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE     1 (bases 1 to 579)
AUTHORS       Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
              Geisel,S., Kucaba,F., Lacy,M., Le,M., Martin,J., Morris,M.,
              Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
              Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
              Waterston,R.
TITLE         The WashU-HMMI Mouse EST Project
JOURNAL       Unpublished (1996)
COMMENT       Contact: Marra M/Mouse EST Project
              WashU-HMMI Mouse EST Project
              Washington University School
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watson.wustl.edu
              This clone is available royalty-free through LLNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:392971
Seq primer:   -28M13 rev2 from Amersham
High quality sequence stop: 495.
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3']; double-stranded cDNA was ligated to Eco RI adaptors
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provided by Dr. Berstrand Jordan. Library went through two
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Soares and M.Fatima Bonaldo."
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ORIGIN

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QY  63 GTGGGGGTGGAGTGGGACAAGGGAAGGGGTGAATGTAAGTCTGATCATCACACCTCTGG 122
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Db   255 GTGGGGGTGGGATGGTGGTGGTATGATGAAGCATGGTCTGGATCTACATGCANGGG 196

QY  123 Tgctgcctccccc 135
||||| ||||| |||||
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DEFINITION 5' similar to gb:Z3090 HEAT SHOCK 27 KD PROTEIN (HUMAN);, mrna
sequence.
ACCESSION AA293284
NID       g1941566
KEYWORDS  EST.

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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;  
Homo.  
REFERENCE 1 (bases 1 to 544)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,  
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
TITLE WashU-Merck EST Project 1997  
JOURNAL Unpublished (1997)  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
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M.Fatima Bonaldo."  
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